

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:54:20 ; Search time 52.3933 Seconds
(without alignments)
1592.744 Million cell updates/sec

Title: US-09-805-550-2

Perfect score: 2036
Sequence: 1 MRLNVKTLKGTNFEIASP.....ELTANYLLDHGHEPDDQQ 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIA:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1211.5	59.5	389	10	Q9STA6	Q9sta6 lycopersico
2	1199.5	58.9	378	10	Q9PFI6	Q9pfi6 arabidopsis
3	1198.5	58.9	378	10	Q9AC35	Q9ac35 arabidopsis
4	1188.5	58.4	419	10	Q9M87	Q9m87 arabidopsis
5	1187.5	58.3	382	10	Q03990	Q03990 daucus caro
6	1127	55.4	392	10	Q40742	Q40742 oryza sativ
7	944.5	46.4	365	10	Q9ACE9	Q9ace9 arabidopsis
8	925.5	45.5	379	10	Q03991	Q03991 daucus caro
9	840.5	41.3	367	10	Q9MA10	Q9ma10 arabidopsis
10	832	31.0	409	4	Q8WDB0	Q8wdb0 homo sapien
11	533	26.7	246	10	Q9S9L8	Q9s9l8 arabidopsis
12	501	24.6	341	5	Q97135	Q97135 dictyostell
13	481	23.6	414	5	Q9V3W9	Q9v3w9 drosophila
14	478	23.5	414	5	Q9XZ60	Q9xz60 drosophila
15	436.5	21.4	372	5	Q23451	Q23451 caenorhabdi
16	376.5	18.5	748	6	P79370	P79370 oryctolagus

17	361.5	17.8	113	10	Q9SA20	Q9sa20 arabidopsis
18	317	15.6	290	5	Q9VCD5	Q9vcd5 drosophila
19	271	13.3	65	10	Q9SCA8	Q9scA8 lycopersico
20	243	11.9	575	10	Q9FWF5	Q9fwf5 oryza sativ
21	231.5	11.4	551	10	Q9AC51	Q9ac51 arabidopsis
22	229.5	11.3	582	10	Q9STI8	Q9sti8 arabidopsis
23	222	10.9	582	11	Q9JUP9	Q9jup9 ratius norv
24	214.5	10.5	523	5	Q9NIF3	Q9nif3 dictyostell
25	213	10.5	582	11	Q8R317	Q8r317 mus musculu
26	210	10.3	538	10	Q9S1I9	Q9s1i9 arabidopsis
27	210	10.3	595	6	Q95M59	Q95m59 bos tauris
28	209	10.3	582	11	Q9QZM1	Q9qzm1 mus musculu
29	202.5	9.9	502	5	Q18672	Q18672 caenorhabdi
30	197.5	9.7	536	11	Q99NB8	Q99nb8 mus musculu
31	197	9.7	589	4	Q9UMX0	Q9umx0 homo sapien
32	196	9.6	601	4	Q9NRR5	Q9nrr5 homo sapien
33	193	9.5	142	10	Q9LEP19	Q9lep19 arabidopsis
34	193	9.5	589	4	Q9HOT8	Q9hot8 homo sapien
35	184.5	9.1	638	11	Q9QZM0	Q9qzm0 mus musculu
36	180	8.8	589	4	Q9H3R4	Q9h3r4 homo sapien
37	179.5	8.8	101	5	Q9GZJ7	Q9gzj7 hydractinia
38	166.5	8.2	624	4	Q9UHD9	Q9uhd9 homo sapien
39	166.5	8.2	624	4	Q9HAZ4	Q9haz4 homo sapien
40	164.5	8.1	1022	5	Q96073	Q96073 drosophila
41	159.5	7.8	1931	10	Q8W2U3	Q8w2u3 oryza sativ
42	158	7.8	545	5	Q9TX05	Q9tx05 caenorhabdi
43	157.5	7.7	314	4	Q9H8R7	Q9h8r7 homo sapien
44	157.5	7.7	585	13	Q9PVN8	Q9pvn8 xenopus lae
45	157	7.7	1527	3	Q8WZ15	Q8wz15 yarrowia li

ALIGNMENTS

RESULT 1

ID Q9STA6 PRELIMINARY; PRT; 389 AA.
AC Q9STA6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE RAD23 protein.
GN RAD23.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. WEST VIRGINIA 106; TISSUE=FRUIT;
RA Lemaire-Chamley M., Petit J., Raymond P., Chevalier C.,
RT "Analysis of gene expression during early tomato fruit development by
RT mRNA differential display."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ243875; CAB51544.1; -
DR HSSP: P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRPFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIDUTIN_2; 1.
SQ SEQUENCE 389 AA; 41508 MW; D2BAEDFOFE70778A CRC64;

Query Match 59.5%; Score 1211.5; DB 10; Length 389;

Best local similarity 63.0%; Pred. No. 14e-65;

Matches 255; Conservative 43; Mismatches 88; Indels 19; Gaps 6;

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DB 1 MKLEFVTLGTHFELEVKEDSVADYKKNIESVQGDVYPAQOMLIHOGKVLKDTTLE 60
OY 61 SNGVAENSFVIMLSKAKASSGASATATAKAPATLAQAPAPVAPASVARTPTQ 117
DB 61 EKKVAENSFVIMLSKKNKVSSTG--TSSISALSNFQAQDGSMDARQRTTTPQAVTALP 118
OY 118 VATAETAPPSVQQAAPATVAATDADVYQAASNLVGNNEEOTIOOILDMGGTWER 177
DB 119 QSASESAP--TPAPVPAASST--DYDDAASNLVAGSNLETTVOOILDMGGGSMDR 172
OY 178 DTVVRLRAAYNNPERAIDYLSGIPENVEAOPVAPAAQGTQNOAASPAQAVATLPV 237
DB 173 DTVVRLRAAYNNPERAAYVLYSGIPETEPVAPAPATVAPASQALINPAQADS 232
OY 238 QSPASAPGPNANPLNLFPGVPSGSGNPGVPGSGALDALRQLPQFALLQVQANQ 297
DB 233 QLAVPSGSGPNANPLDLPQGLTNAGSN-----AGAGNLDFLRNSQFQALRAMVQANQ 286
OY 298 IIOQPMLOELGKONPOLRIQENQAEFLRLVNESPGSGGNGILQALAAVPOTLVTPE 357
DB 287 IIOQPMLOELGKONPOLRIQENQAEFLRLVNESPGSGGNGILQALAAVPOTLVTPE 344
OY 358 EREARLORLEGMGFNELVEVFPACNKDELTANVLLDHGHEFDQ 402
DB 345 EREARLORLEGMGFNELVEVFPACNKDELTANVLLDHGHEFDQ 389

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RESULT 2

O9F16 PRELIMINARY: PRT: 378 AA.

AC 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE DNA repair protein RAD23 homolog (Hypothetical 40.1 kDa protein)
 DE (A5538470/At5g38470).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 RX NCBI_Taxid=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=97471969; PubMed=9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneo T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT pl clones.";
 RL DNA Res. 4:215-230(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onda C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onda C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

RA Ecker J.R.;
 RT "Arabidopsis ORF clones.";
 RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB005248; BAB09359.1;
 DR EMBL: AY058196; BAL25609.1;
 DR EMBL: AY081835; AAL87405.1;
 DR HSP: P54725; IDVO;
 DR InterPro: IPR004806; Rad23.
 DR InterPro: IPR004449; UBA_domain.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00627; UBA_2.
 DR Pfam: PF00240; Ubiquitin_1.
 DR SMART: SM00165; UBA_2.
 DR SMART: SM00213; UBQ_1.
 DR TIGRFAMs: TIGR00601; rad23_1.
 DR PROSITE: PS0053; UBIQUITIN_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 378 AA; 40066 MW; DD9B59135EA366A9 CRC64;

Query Match 58.9%; Score 1199.5; DB 10; Length 378;
 Best Local Similarity 62.9%; Pred. No. 7.1e-65;
 Matches 256; Conservative 43; Mismatches 75; Indels 33; Gaps 9;

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OY 1 MKLVNLTGTHFELEVKEDSVADYKKNIESVQGDVYPAQOMLIHOGKVLKDTTLE 60
DB 1 MKLEFVTLGTHFELEVKEDSVADYKKNIESVQGDVYPAQOMLIHOGKVLKDTTLE 59
OY 61 SNGVAENSFVIMLSKAKASSGASATATAKAPATLAQAPAPVAPASVARTPTQ 116
DB 60 ENNVENSFVIMLSKTKASSGASATAPAPATQPVATPQVS-APTASV----- 111
OY 117 PVATETAPPSVQQAAPATVAATDADVYQAASNLVGNNEEOTIOOILDMGGTWER 176
DB 112 PVPTSGTA-----TAAAP--TAAVQTVYGGQAASNLVAGTLESTVOOILDMGGGSMD 164
OY 177 RDTVVRLRAAYNNPERAIDYLSGIPENVEAOPVAPAAQGTQNOAASPAQAVATLP 236
DB 165 RDTVVRLRAAYNNPERAAYVLYSGIPAEIIPVAAQAPATGQANPLAQPOQAAA--- 221
OY 237 VOPSPASAPGPNANPLNLFPGVPSGSGNPGVPGSGALDALRQLPQFALLQVQANP 296
DB 222 --PAATGCGPNANPLNLFPGQMPAADA-----GAGAGNLDFLRNSQFQALRAMVQANP 273
OY 297 QILOPMLOELGKONPOLRIQENQAEFLRLVNESPGSGGNGILQALAAVPOTLVTPT 356
DB 274 QILOPMLOELGKONPOLRIQENQAEFLRLVNESPGSGGNGILQALAAVPOTLVTPT 331
OY 357 EREARLORLEGMGFNELVEVFPACNKDELTANVLLDHGHEFDQ 403
DB 332 EREARLORLEGMGFNELVEVFPACNKDELTANVLLDHGHEFDQ 378

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RESULT 3

O94C35 PRELIMINARY: PRT: 378 AA.

AC 094C35;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 40.1 kDa protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 RX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Shinn P.,
 RA Bowser L., Carninci P., Bowser L., Carninci P., Chung M.K.,
 RA Tracy S.E., Banh J., Bowser L., Carninci P., Jones T., Kamiya A.,
 RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
 RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,

RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY037181; AAK59766.1; -
DR InterPro: IPR00449; UBA.domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR TIGRPFAM: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 40075 MW; E49B591527A3EC27 CRC64;

Query Match 58.9%; Score 1198.5; DB 10; Length 378;
Best Local Similarity 62.9%; Pred. No. 8.2e-65;
Matches 256; Conservative 43; Mismatches 75; Indels 33; Gaps 9;

QY 1 MKLVNKLKGTNFEIENASPDASVADYKRIETTGOGSTYRADOQMLYQKILKDETTLE 60
DB 1 MKLVNKLKGTNFEIENASPDASVADYKRIETTGOGSTYRADOQMLYQKILKDETTLE 59
QY 61 SNGVAENSFLVIMLSKAKSSGASTAT--TAKAPATIAQAPAPAPAPAPAPARTTQA 116
DB 60 ENNVNENSVFLVIMLSKAKSPASSTASAPAPATQPTQATATQVS-APTASV----- 111
QY 117 PVAETAETAPSPVQAPAPATVATDDADYVSOAASNLVFGNNIECTIQOILDMGSGTWE 176
DB 112 PVTTSIGA-----TAAAPA--TAASVOTDYGAASNLVAGTILLESVQOILDMGSGSWD 164
QY 177 RDTVVRALRAAYNNPERAIDYLSGIPENVEAOPVARAPAGQOTNOAASPAQAVPALP 236
DB 165 RDTVVRALRAAYNNPERAIDYLSGIPENVEAOPVARAPAGQOTNOAASPAQAVPALP 221
QY 237 VQSPASAGNANPLNFPQGVSPSGSNPGVVGAGSGALDALROLPQFALLQVQANP 296
DB 222 --PAAATGGNANPLNFPQGVMPADA-----GAGAGNLDLFLNSHOFALRLAMVQANP 273
QY 297 QILQPMLOELGKONPOLILRIQENQAEFLRLVNESPEGPGCNILGOLAAVPOTLVTP 356
DB 274 QILQPMLOELGKONPOLILRIQENQAEFLRLVNESPEGPGCNILGOLAAVPOTLVTP 331
QY 357 EEBEATIQLEGMGFNRELVEVEFACNKEDELTANYLLDHGHEFDDQ 403
DB 332 EEBEATIQLEGMGFNRELVEVEFACNKEDELTANYLLDHGHEFDDQ 378

RESULT 4
Q9M887 PRELIMINARY; PRT; 419 AA.
AC Q9M887;
DT 01-OCT-2000 (TREMUREL. 15, Created)
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
DE 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE Putative RAD23 (AT3902540/F16B3_17).
GN F16B3.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Rowan C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome YI BAC F16B3 genomic sequence";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

RA Bowser L., Carinci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC021640; AAF32461.1; -
DR EMBL: AY039562; AAK62617.1; -
DR HSSP: P54725; IDVO.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR00449; UBA.domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBQ; 1.
DR TIGRPFAM: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIQUITIN_2; 1.
SQ SEQUENCE 419 AA; 44247 MW; CAA13BC4FFB1E25 CRC64;

Query Match 58.4%; Score 1188.5; DB 10; Length 419;
Best Local Similarity 58.4%; Pred. No. 3.7e-64;
Matches 253; Conservative 53; Mismatches 82; Indels 45; Gaps 10;

QY 1 MKLVNKLKGTNFEIENASPDASVADYKRIETTGOGSTYRADOQMLYQKILKDETTLE 60
DB 1 MKLVNKLKGTNFEIENASPDASVADYKRIETTGOGSTYRADOQMLYQKILKDETTLE 60
QY 61 SNGVAENSFLVIMLSKAKSSGASTAT--TAKA-----PATIAQAPAPAP 105
DB 61 ENKVAENSFLVIMNKKSKPASAASAGTSQAKSLPSTQSPSTPQTPASVAPAR 120
QY 106 AAS-----VARTPTQAPVATETAPPSVQAPAPATVAT-----DDADYVSOAS 152
DB 121 APTPPPPAPPTPPAPVATETVTPPI-PEVPATISSPTAPDASVSGDVGQAS 179
QY 153 NLVYGNLLEQTOOILDMGGTWERDLYVRLRAYNNPERAIDYLSGIPENVEAOPVA 212
DB 180 NLVYGNLLEQTOOILDMGGTWERDLYVRLRAYNNPERAIDYLSGIPENVEAOPVA 239
QY 213 RAPAGQOTNOAASPAQAVPALPVPQSPASAGNANPLNFPQGVSPSGSNPGVVGAG 272
DB 240 RPPASAGQAPAPAPATQTPAAA-----PAS-GPNANPLDLFPGLPVGGNP-----G 286
QY 273 SGALDALROLPQFALLQVQANPOLILQPMLOELGKONPOLILRIQENQAEFLRLVNESP 332
DB 287 AGTLDLFLNSQGFQALRAMVQANPOLILQPMLOELGKONPNLMRLIOHQADFRLINEPV 346
QY 333 E-GGPGNIIQGLAAAY--POTLTVPBEERAIQRLGGMGFNRELVEVEFACNKEDELT 389
DB 347 EGGESESNLIGQMAAGPQALQIVTHERERAIQRLGGMGFNRELVEVEFACNKEDELA 406
QY 390 ANYLLDHGHEFDD 402
DB 407 ANYLLDHGHEFEE 419

RESULT 5
O03990 PRELIMINARY; PRT; 382 AA.
AC O03990;
DT 01-JUL-1997 (TREMUREL. 04, Created)
DT 01-JUL-1997 (TREMUREL. 04, Last sequence update)
DE 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE RAD23, Isoform I.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OX Asteridae: euasterids II; Apiales; Apilaceae; Daucus.
 OC NCBI_TaxID=4039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MO01C;
 RX MEDLINE=98345997; PubMed=9681019;
 RA Sturm A., Leinhard S.;
 RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in
 RL Plant J. 13:815-821(1998).
 DR EMBL: Y12013; CAAT741.1.; -.
 DR HSSP: P54725; IDVO.
 DR InterPro: IPR004486; Rad23.
 DR InterPro: IPR000449; UBA domain.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00627; UBA; 2.
 DR Pfam: PF00240; ubiquitin; 1.
 DR SMART: SM00165; UBA; 2.
 DR SMART: SM00213; UBO; 1.
 DR TIGRFAMs: TIGR00601; rad23; 1.
 DR PROSITE: PSS0053; UBQUITIN_2; 1.
 SO SEQUENCE 382 AA; 40344 bp; 27FF02A2402F3DC2 CIRC64;

Query Match	58.3%;	Score 1187.5;	DB 10;	Length 382;
Best Local Similarity	62.7%;	Pred. No. 3.8e-64;		
Matches 255; Conservative	46;	Mismatches 75;	Indels 31;	Gaps 11

Oy	1	MKLAVKTLKGNFLEASPDVADYKRILETTGOSGYRADOOMLTGGKILKEDETFLE	60
Db	1	MKIYVKTLKSQFELQYNPDDSVADVRSIETAGAAVYPAQGMILTYGSKVLKDGTLL	60
Oy	61	SNGVAENSEFLYMISKAASSSGASTATTA---KAPITLQPAAPAIPAASVARTPPQAP	117
Db	61	ENNAENSEFLYMISKSSPSGEGSTTSTAAPAPPTSAAPSPV-APAS-----QP	113
Oy	118	VATAET-AP-PSVOPOAAPATVATDADADYQSQAASNLVFNGNLTQITQIIDMGCGTW	175
Db	114	ASTLPVPASPAPATAPATPIISAASVGSEANYDSABSLVAGNSLBEALIQIIDMGGTWM	173
Oy	176	ERDYVVALRAAYNNPEALIDYLTSGITPENVEAOAPAARAAGCQTQOQAASPA-QPAVA	234
Db	174	DRDYIVIRVRAAFNPPEAVEYEYLSGIEQAEAPPVAPSPEG----QAANPLDQPPAA	228
Oy	235	LPVOPSPASAPNANPLNTLFQOGVPSGSGNPGVYPGAGSGLDALRLQPFQALILDVQA	294
Db	229	--AGAPASAPNANPLDLFPQGLPDMGSN-----AAGACGLDPLRTNQGFQALRAYQS	281
Oy	295	NPOLIQLJOLGLGNQRIILFTIOENQAEPLRLVNESPEGSGGNIIIGOLAAAVPQTLTV	354
Db	282	NPOLIQPMQLDELGNQNPLMLTLIEHOADFQILINMEPEG--NILGH-----GPQAVIS	335

```
OY      355 TPPEEREAIORLEGMGFNRELVLVEFFACNKNDEELTANYLLDHGHEED 401
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB       336 TPEERDATELEANGFDRELVLVEFFACNKNNEELANYLLDHNHREE 382
```

RESULT	6		
040742			
ID	040742	PRELIMINARY:	PRT: 392 AA.
AC	040742:		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	OSRAD3.		
OS	Oryza sativa (Rice).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCHI_TaxID=4530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NIPPONBARE;		
EX	MEDLINE=97369378; PubMed=9225866;		

RA Schultze T.F., Quattrano R.S.:
RT "Characterization and expression of a rice RAD23 gene.";
RL Plant Mol. Biol. 34:557-562(1997).
DR EMBL; U63530; AAB5841.1; -.
DR HSSP; P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBQ; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS00053; UBQUITIN_2; 1.
SQ SEQUENCE 392 AA; 41754 MW; BDE08574ACCTACB CRC64;

Query Match	55.4%	Score 1127;	DB 10;	Length 392;
Best Local Similarity	59.1%;	Pred. No. 1.8e-60;		
Matches 243;	Conservative 48;	Mismatches 90;	Indels 30;	Gaps 9;

[illegible]

RESULT 7
Q94CE9
ID Q94CE9 PRELIMINARY; PRT; 365 AA

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative RAD23 protein.
GN F20B17.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eumaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Iiu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bowers J., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamliya A., Karlin-Neumann G., Kawai J., Kim C., Koeseema E.,
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sekurai T., Satou M., Seki M., Shim P., Southwick A.,
RA Shinohashi K., Davis R.W., Ecker J.R., Theologis A.,
RT *Full length cDNA of gene F20B17.8 (GI:7715605) ;

RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
 RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carrinot P., Chen H., Cheuk R.,
 RA Hayashitaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koeseke E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full length cDNA of gene P20B17.8 (GI:7715605).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY034912; AAK59419.1; -;
 DR EMBL: AY063103; AAL34277.1; -;
 DR InterPro: IPR004806; Rad23.
 DR InterPro: IPR000449; UBA.domain.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00627; UBA; 2.
 DR Pfam: PF00240; ubiquitin; 1.
 DR TIGRFAMs: TIGR00601; rad23; 1.
 DR PROSITE: PS50053; UBIOUITIN_2; 1.
 SQ SEQUENCE 365 AA; 39157 MW; 4FED9EC59B467745 CRC64;

Query Match 46.4%; Score 944.5; DB 10; Length 365;
 Best Local Similarity 50.5%; Pred. No. 1.7e-49;
 Matches 206; Conservative 56; Mismatches 97; Indels 49; Gaps 9;
 QY 1 MKNLVTKLGTNEIEASPDASVADYVKRIETTOGOSTYRADQMLYOGKILKDETTLE 60
 DB 1 MKNLVTKLGTNEIEASPDASVADYVKRIETTOGOSTYRADQMLYOGKILKDETTLE 60
 QY 61 SNGVAENSEFLVIMSKAKA-SSSGASTATTAKAPATLAQPAAPAPASVARTPTQAPVA 119
 DB 61 ENKVTGEGLVLMGSKTSKSGSAGASVQVYSATFTSTKRAAP-----STTQSSPV 111
 QY 120 TATTAAPSVOQAAPATVAATDADYVSCAASNLVFGNNLEQTLQOILDMGGTWERDT 179
 DB 112 PAPTAPQEDPAA-----QTPDYGQAASLTIVSGSSLEDMVQOIMEMGGGSMKET 161
 QY 180 VVALRAAYNNPERAIDYLSGIPENVE-AQPARAPAGQQTNOQAASPAQPAVALPVQ 238
 DB 162 VVALRAAYNNPERAIDYLSGIPENVE-AQPARAPAGQQTNOQAASPAQPAVALPVQ 238
 QY 239 PSPASAGPNANPLNLFPGVPSGSGSNPGVYPGAGS--GALDALRQLPQFQALQLQVQAN 295
 DB 208 -APASGGPNSPLDLPQ-----ETVAAAGSGDLGTLFELRNNDQFQALRTVHSN 257
 QY 296 POLQPMLEIGKONPOLRLIOENQAEFLVNESPEGGPG-GNIIQOLAAYVPTLVPE 354
 DB 258 POLQPMLEIGKONPOLRLIOENQAEFLVNESPEGGPG-GNIIQOLAAYVPTLVPE 317
 QY 355 TPPEAREIORLEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 402
 DB 318 TPPEAREIORLEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 365

RESULT 8
 ID 003991 PRELIMINARY; PRT; 379 AA.
 AC 003991;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RAD23 protein, isoform II.
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids II; Apiales; Apiales; Daucus.
 OX NCBITaxID=4039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M001C;

RX MEDLINE=98345997; PubMed=9681019;
 RA Sturm A., Leinhard S.;
 RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in
 RT yeast.";
 RL Plant J. 13:815-821(1998).
 DR EMBL: Y12014; CAA72742.1; -;
 DR HSSP: P54725; IDV0.
 DR InterPro: IPR004806; Rad23.
 DR InterPro: IPR000449; UBA.domain.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00627; UBA; 2.
 DR Pfam: PF00240; ubiquitin; 1.
 DR SMART: SM00165; UBA; 2.
 DR SMART: SM00213; UBA; 1.
 DR TIGRFAMs: TIGR00601; rad23; 1.
 DR PROSITE: PS50053; UBIOUITIN_2; 1.
 SQ SEQUENCE 379 AA; 40530 MW; B26697BA39CC5929 CRC64;

Query Match 45.5%; Score 925.5; DB 10; Length 379;
 Best Local Similarity 50.2%; Pred. No. 2.4e-48;
 Matches 203; Conservative 57; Mismatches 117; Indels 27; Gaps 8;
 QY 1 MKNLVTKLGTNEIEASPDASVADYVKRIETTOGOSTYRADQMLYOGKILKDETTLE 60
 DB 1 MKNLVTKLGTNEIEASPDASVADYVKRIETTOGOSTYRADQMLYOGKILKDETTLE 60
 QY 61 SNGVAENSEFLVIMSKAKA-SSSGASTATTAKAPATLAQPAAPAPASVARTPTQAPVA 119
 DB 61 ESKISEDEGLVLMGSKTSKSGSAGASVQVYSATFTSTKRAAP-----STTQSSPV 120
 QY 120 TATTAAPSVOQAAPATVAATDADYVSCAASNLVFGNNLEQTLQOILDMGGTWERDT 179
 DB 121 TVPAP--LSPAPAP-----SDTYGEAASNVVAGSNLEQTLQOILDMGGGMMPTNM 169
 QY 180 VVALRAAYNNPERAIDYLSGIPENVEAQ-PVARAPAGQQTNOQAASPAQPAVALPVQ 238
 DB 170 VVALRAAYNNPERAIDYLSGIPENVEAQ-PVARAPAGQQTNOQAASPAQPAVALPVQ 223
 QY 239 PSPASAGPNANPLNLFPGVPSGSGSNPGVYPGAGS--GALDALRQLPQFQALQLQVQAN 298
 DB 224 -GAAPAPNSPLNLFPGVPSGSGSNPGVYPGAGS--GALDALRQLPQFQALQLQVQAN 276
 QY 299 LQPMLEIGKONPOLRLIOENQAEFLVNESPEGGPGGNIQOLAAYVPTLVPE 358
 DB 277 LQPMLEIGKONPOLRLIOENQAEFLVNESPEGGPGGNIQOLAAYVPTLVPE 335
 QY 359 REAIORELEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 402
 DB 336 REAIORELEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 379

RESULT 9
 ID 09MA10 PRELIMINARY; PRT; 367 AA.
 AC 09MA10;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE P20B17.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBITaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
 RA Shin P., Altati H., Bel Q., Chin C., Chio J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;

*Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome 1.
RT 1.
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bel B., Chin C., Chlou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thayer A., Tortum M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC010793; AAF68123.1; -
DR HSSP; P54725; IDV0.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00627; UBA; 2.
DR SMART; SM00240; ubiquitin; 1.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBO; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 367 AA; 39790 MW; C6D01134B5C69CE6 CRC64;

Query Match 41.3%; Score 840.5; DB 10; Length 367;
Best Local Similarity 47.4%; Pred. No. 3.1e-43;
Matches 192; Conservative 53; Mismatches 119; Indels 41; Gaps 8;

QY 1 MKLVNLTGKTFEIASPDASVADYKRIETTGOGSTYRADOQMLYQKILKDETTLE 60
DB 1 MKLVNLTGSHFEIRIVLPSDITMAVKNIEDSGKDNPCGGQQLIHNGKYLKDETSLV 60
QY 61 SNGVAENSEFLVIMLSKAKSSSGASTATTAKAPATLAQAPAPAPAPASVARTPTQAPVAT 120
DB 61 ENKVEEGFLVWLKSKSGS---AGQASVOCVRLFLHSLFPLPHLSIYVPET 116
QY 121 AETAPPSVOPAPAPATVATDADVYSQAASNLVGNMLEQTIQIILMGCGTWERDVI 180
DB 117 GCGFTYS-----CRTGTGTDTYGAASATLYSGSSLEQWVQIMEMGSGMDKETV 166
QY 181 VNALRAAYNNPERAIDLYSGIPEVNE-AQPVARAPAGQQTNOQASPAQAPVALVPQ 239
DB 167 TATLRAAYNNPERAIDLYSGIPEVNE-AQPVARAPAGQQTNOQASPAQAPVALVPQ 211
QY 240 SPASAGPNANPLNLPFGVPSGSGSNQGVPPAGSGALDLRLQ-LPQFALLQVQANPQI 298
DB 212 APASGPNNSPLDLPQ-----ETVAAAGSGDLGLLELRNNDQVAIITISAFSLN 262
QY 299 LQPMLOELGKQNPQILRLIQENQAEFLRLVNESPEGGPG-GNLIQGLAAVAPQTLVTE 357
DB 263 CEPMLQELGKQNPQILRLIQENQAEFLRLVNESPEGGPG-GNLIQGLAAVAPQTLVTE 322
QY 358 EBEAIORELGKGNRELVEFPACNKDELTANYLLDHGHEFD 402
DB 323 EBEAIORELGKGNRELVEFPACNKDELTANYLLDHGHEFD 367

RESULT 10
Q8WUB0 PRELIMINARY; PRT; 409 AA.
Q8WUB0;
AC 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE RAD23 homolog B (S. cerevisiae).
OS Homo sapiens (Human).
OC Eukaryota; Eutezoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020973; AAH20973.1; -
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR000449; UBA_domain.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBO; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 409 AA; 43199 MW; 475FBD499DACAC69 CRC64;

Query Match 31.0%; Score 632; DB 4; Length 409;
Best Local Similarity 34.5%; Pred. No. 1.3e-30;
Matches 153; Conservative 81; Mismatches 133; Indels 76; Gaps 12;

QY 1 MKLVNLTGKTFEIASPDASVADYKRIETTGOGSTYRADOQMLYQKILKDETTLE 60
DB 1 MOYTKTLQOQTFKIDIDDEETVKAKEIKESKGDAPVAGQKILTAGKILNDTALK 60
QY 61 SNGVAENSEFLVIMLSKAKSSSGASTATTAKAPATLAQAPAPAPASVARTPTQAPVAT 109
DB 61 EKKIDENFVVMVTKPKAVSTIPAPATQOSAPASTTAVTSSTTTVAAPIPV-PALAP 119
QY 110 ARTPTQ-----APVATETAPPSVOPQAPAPAT-VAATDD-----ADVTSQ 149
DB 120 TSPASITPASATASSEPAPASAKOEKPAETPAETPAETPAETPAETPAETPAETPAET 179
QY 150 AASNLVFGNNLQOTIQLIDMGCGTWERDVIYRALRAAYNNPERAIDLYSGIPEVNEAO 209
DB 180 AITSALVTGSGYENMTYELSMG---YERQVYIALRASNNPDRAVETLMLKIPDRESQ 236
QY 210 PVARAPAGQQTNOQAS---PAQAPVALVPQSPASAGPNANPLNLPFGVPSGSGSNQ 266
DB 237 AYVADP-----QAASGVPOSSAVAAAATTAT-----TTSSGGHP- 275
QY 267 VPPAGSGALDLRLQPOLQVQANPQILQPMLOELGKQNPQILRLIQENQAEFLR 326
DB 276 -----LEFLRNQPOQORQIIONPSLLPALQOIGRENQOLLOISQHOEHFIQ 326
QY 327 LVNE-----SPGGPGGNLIQGLAAV---QTLVYTPPERAIOIRLBSGMFRELVEV 378
DB 327 MLNEPQVQAGGGGGGGGGGSIAGSGHMYIOTVPOEKATIERALGPEGLVIOA 386
QY 379 FFACNKDELTANYLLDHGHEFD 401
DB 387 YFACENKELNLANPLQGNFDD 409

RESULT 11
Q9S9L8 PRELIMINARY; PRT; 246 AA.
Q9S9L8;
AC 09S9L8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE T24D18.27 protein.
GN T24D18.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Ienz C., Pham P.,
RA Tortumli M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Howing B., Koo T., Li J., Liu A., Vaysberg M., Altali H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shin P., Tambunga G.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT *The sequence of BAC T2418 from Arabidopsis thaliana chromosome 1.*;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC010924; AAF18513.1; -.
DR HSSP: P02248; 1UBI.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 1.
DR SMART: SM00213; UBO; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
DR SEQUENCE 246 AA; 25966 MW; 0867D1E7D72B6FEE CRC64;
SQ
Query Match 26.7%; Score 543; DB 10; Length 246;
Best Local Similarity 41.8%; Pred. No. 1.7e-25;
Matches 117; Conservative 41; Mismatches 74; Indels 48; Gaps 4;
QY 1 MKLWVKTLKGNFIEASPDASVADVVRRIETTGOGSTYRADQOMLYOGKILNDETTLE 60
DB 1 MKLVKTKLKGSHREIVLPDTIMAVKKNIEDSGKDNYPGCGQLLHNGKVLKDETTLY 60
QY 61 SNGVAENSFLVIMLSKAKASSGASTATTAKAPATLAQPAAPVAPASVARTPPQAPVAT 120
DB 61 ENRYTEGFLVIMLSKSKTASAGPSTQLAAPSTQSIIVPASPNSPPVOEOPFA----- 115
QY 121 AETAPSPVQAPAPATVATTDADVYSOASNLVFGNNLEOTQOILIDMGCGTWERTV 180
DB 116 -----QSDITYGQASSTIVSGSSSTEQOMYQQLMEKGGSWDKETV 153
QY 181 VRALRAAYNNPERAIDLYSGIPENVEAPARAPAAQOQTNOQAPAPPAVALPYQPS 240
DB 154 TRALRAAYNNPERAVDLYSGIPETV---TTPATNLSGVSGRELTAPE----- 198
QY 241 PASAGPAPNAPLNFPGQVPSGGSNPGVYPGAGCALDALR 280
DB 199 PPSGGPNSPLDLFPPQAVSDAA-----GGDILGTLLEFLR 232
RESULT 12
ID 097135 PRELIMINARY; PRT; 341 AA.
AC 097135;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Repc-binding protein A.
GN RCBA.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLB153;
RA Li G., Alexander H., Alexander S.;
RT *rcba, the Dictyostelium discoideum homolog of yeast repair gene
RAD23.*;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF103870; AAD17913.1; -.

DR HSSP: P54725; 1DV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
DR SEQUENCE 341 AA; 37528 MW; E376B909E6EDE57E CRC64;
SQ
Query Match 24.6%; Score 501; DB 5; Length 341;
Best Local Similarity 31.9%; Pred. No. 8.6e-23;
Matches 136; Conservative 59; Mismatches 123; Indels 108; Gaps 15;
QY 1 MKLWVKTLKGNFIEASPDASVADVVRRIETTGOGSTYRADQOMLYOGKILNDETTLE 60
DB 1 MKVTIKNKKEIYFEVANGDLTVALKNLISEKHNT---PSWOTLLYSGKILDEKRTLE 57
QY 61 SNGVAENSFLVIMLSKAKASSGASTATTAKAPATLAQPAAPVAPASV----- 109
DB 58 SYNTDGGFLKMKTKPR-----EAPAT--TPASTPPLNTYSTNNHHYCRT 103
QY 110 -----ARPTQAPVATTAETAPPVQAPAPATVATDADVYSOASNLVFGN 158
DB 104 NPNHKLNNSTTPTTSVPPTNNNT-PATPNPTTSTSPGSTTS--PQSSDFATGT 160
QY 159 NLKGTQOILIDMGCGTWERTVVALRAAYNNPERAIDLYSGIPENVEAPARAPAG 218
DB 161 ELETKINKITMG--PARDQVLAALRTFNNAAREALEYVSG-----NIPAN 206
QY 219 QOTNOQASAPAPAPVALPVQSPASAGPAPNAPLNFPGVPSGGSNPGVAPAGSALDA 278
DB 207 DPEDDEE-----MEGCG-----GSDNPFEE 227
QY 279 LRQLPQFQALQLVQANPQILQPMQLQELGKONPQILRTIOENQAEFLVNESPEGGG 338
DB 228 LRNPHEFLRLREALISKNSIIPGILQIAQTNPALVRQIQENPMEFLTF--QGDGNGCG 285
QY 339 NILQGLAAVYQTLVNPDEEAREATORLEGM--GFRRELVEVFPKCNDELTAVYLDHG 397
DB 286 N-PGQF-----TLQVQSESEAIORLQALGMDKSTVIEAFACDNKEELTASYLFETA 338
QY 398 HEFDDQ 403
DB 339 ---DDE 341
RESULT 13
ID 09V3W9 PRELIMINARY; PRT; 414 AA.
AC 09V3W9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE RAD23 protein.
GN RAD23 OR CG1836.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blatej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.T.G.,

RA Abri1 J.F., Agbayeni A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,
RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Boriva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostali M., Kallush F., Karpen G.H., Ke Z., Kennison J.P., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Pacled J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).

RP SEQUENCE FROM N.A.
RA Brodsky M.H., Rubin G.M., Tsang G.;
RT "Full Length Drosophila melanogaster cDNA sequence.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003844; AAF59352.1; -;
DR EMBL: AF132147; AAD33594.1; -;
DR HSSP: P54725; IDV0.
DR Flybase: FBgn0026777; Rad23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiqultin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiultin; 1.
DR PRINTS: PR01574; TUBBYPROTEIN.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 414 AA; 45780 MW; 4C2E494CA116F7AB CRC64;

Query Match 23.6%; Score 481; DB 5; Length 414;
Best Local Similarity 29.3%; Pred. No. 1.8e-21;
Matches 134; Conservative 72; Mismatches 153; Indels 98; Gaps 10;

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DB 1 MTTIKNLQOQFTIEFAFEKTVLELKKIFERGPB-YVAEKOKLIYAGVILTDRTYG 59
OY 61 SNGVAVNSFLVIMLSKAKASSS-----GASTATTAKAPATIAQAPAPAPAPASVARTPT 114
DB 60 SYNDEKKEFIYVMLTRDSSSSNRNOLSVKESNKLITSTDSKOSMPCBEANHTNSPSTNT 119
OY 115 GAVPATAETAPSPVQQAAPATVAATDADVYSGAASNLVFGNNLBOFTIOOILMGCGT 174
DB 120 EDVSVLSRETRPLSSDELLGELA-----QASLQSRASNSLMDGDEYNGTVLSVKEKG--- 170
OY 175 WERDTYVVALRAAYNNPERAIDLYSGIPENVEAOPVAPAPAGOOTNOQAASPAQAPAVA 234
DB 171 YPREGVERAMASYNPNPEAVEYLINGIP-----AEGGTFFYNRLNESTINPSTL 217

OY 235 LPVQSPASAGPNANPLNFPQGVPSGSGSNPGVVPBGASGALDALRQLPQFOALLQVYA 294
DB 218 IBSGPPQASA-----TSAERSTESN-----SDPEEFLNSQPOFLQMSRLIYQ 259
OY 295 NPOILQPMLOELCKONPOLIRLQENQAEFLRLVNE--SPEGPGGNIIGOLAAVAPQTL 352
DB 260 NPHLLHANVLOQIQOTNPALQLQISENQDAFLNMLNPIDRESGATVPVSNARLPSTL 319
OY 353 -----TYTPPERAIOQL 365
DB 320 DWVDLSPDLVATSAQSAAGTSAHQSGAADNEDLQPLGVSTIRLNQDKDAIERL 379
OY 366 EGMGFRELVLVEFFACNNDELTANYLLDRHGFEPD 402
DB 380 KALGFPEALVLQAYFACERNEQANFL--SSSFPD 414

RESULT 14
ID Q9XZE0 PRELIMINARY; PRT; 414 AA.
AC Q9XZE0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE DHR23.
GN RAD23 OR CG1836.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Nabirochkina E.N., Grischuk A.L., Soldatov A.V.;
RT "Cloning and characterization of the Drosophila melanogaster homologue
of the Saccharomyces cerevisiae gene RAD23.";
RL Genetika 35:0-0(1999).
DR EMBL: AF136606; AAD33695.1; -;
DR HSSP: P54725; IDV0.
DR Flybase: FBgn0026777; Rad23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiqultin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiultin; 1.
DR PRINTS: PR01574; TUBBYPROTEIN.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 414 AA; 45794 MW; 4C2FP94CA116F7AB CRC64;

Query Match 23.5%; Score 478; DB 5; Length 414;
Best Local Similarity 29.1%; Pred. No. 2.7e-21;
Matches 132; Conservative 72; Mismatches 154; Indels 96; Gaps 9;

OY 1 MKNVKTILKGNFEIEASPDASVADVKRIIEFTQGSYRADQOMLIYOGKILKDETTLE 60
DB 1 MTTIKNLQOQFTIEFAFEKTVLELKKIFERGPB-YVAEKOKLIYAGVILTDRTYG 59
OY 61 SNGVAVNSFLVIMLSKAKASSS-----GASTATTAKAPATIAQAPAPAPAPASVARTPT 114
DB 60 SYNDEKKEFIYVMLTRDSSSSNRNOLSVKESNKLITSTDSKOSMPCBEANHTNSPSTNT 119
OY 115 GAVPATAETAPSPVQQAAPATVAATDADVYSGAASNLVFGNNLBOFTIOOILMGCGT 174
DB 120 EDVSVLSRETRPLSSDELLGELA-----QASLQSRASNSLMDGDEYNGTVLSVKEKG--- 170
OY 175 WERDTYVVALRAAYNNPERAIDLYSGIPENVEAOPVAPAPAGOOTNOQAASPAQAPAVA 234
DB 171 YPREGVERAMASYNPNPEAVEYLINGIP-----AEGGTFFYNRLNESTINPSTL 217
OY 235 LPVQSPASAGPNANPLNFPQGVPSGSGSNPGVVPBGASGALDALRQLPQFOALLQVYA 294

